




## Evidence for the agricultural origin of antimicrobial resistance in a fungal pathogen of humans

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doi: <https://doi.org/10.1101/2020.05.24.113787>

- Showed that azole-resistant isolates of *A. fumigatus* from *clinical* and agricultural settings also carry mutations conferring resistance to **quinone outside inhibitor (QoI) fungicides, which are used exclusively in agricultural settings.**
- Fourteen (8 agricultural, 6 from patients) of 19 pan-azole-resistant *A. fumigatus* isolates included in the study also carried mutations for QoI resistance
- This is the first report of a clear marker for the agricultural origin of resistance to a clinical antifungal.

# Azole-resistant *Aspergillus fumigatus* in the environment: Identifying key reservoirs and hotspots of antifungal resistance

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Published: July 29, 2021 • <https://doi.org/10.1371/journal.ppat.1009711>

- **Literature review:** the global occurrence of azole-resistant *A. fumigatus* in the environment; interactive world map showing where resistant isolates have been detected and includes information on the specific alleles identified, environmental settings, and azole fungicide use
- Developed environments, specifically hospitals and gardens, were the most common settings where azole-resistant *A. fumigatus* was detected, followed by soils sampled from agricultural settings (~37%). Sampling/reporting bias is likely a factor
- TR<sub>34</sub>/L98H resistance allele was the most common in all regions except South America where the TR<sub>46</sub>/Y121F/T289A allele was the most common.
- Call for increased surveillance to pinpoint reservoirs, need for antifungal stewardship to protect use of antifungals to protect both humans and crops

# Genomic Diversity of Azole-Resistant *Aspergillus fumigatus* in the United States

Authors: [Mona A. Elie](#), [Elizabeth L. Seaton](#), [Lillian C. Lee](#), [Caitlin M. Hogg](#), [David B. Lachance](#), [Karin Beck](#), [J. Kye Drexler](#), [Layana Rodriguez](#) and [Anastasia P. Iliopoulou](#) : [AUTHORS INFO & REFERENCES](#)

DOI: <https://doi.org/10.1128/mbe.00117.21> : [Check for updates](#)



FULL TEXT

PDF/EPUB

- Used whole-genome single nucleotide polymorphism (SNP) analysis on 179 nationally represented clinical and environmental *A. fumigatus* genomes from the United States along with 18 non-U.S. genomes to evaluate the genetic diversity and foundation of the emergence of azole resistance in the United States
- Showed the presence of clades of *A. fumigatus* isolates: clade A (17%) comprised a global collection of clinical and environmental azole-resistant strains, including all strains with the TR<sub>34</sub>/L98H allele from India, The Netherlands, the United Kingdom, and the United States, and clade B (83%) consisted of isolates without this marker mainly from the United States.
- TR<sub>34</sub>/L98H polymorphism was shared among azole-resistant *A. fumigatus* strains from India, The Netherlands, the United Kingdom, and the United States, suggesting the common origin of this resistance mechanism
- Six percent of azole-resistant *A. fumigatus* isolates from the United States with the TR<sub>34</sub> resistance marker had a mixture of clade A and clade B alleles, suggestive of recombination
- Study demonstrates the genetic background for the emergence of azole resistance in the United States, supporting a single introduction and subsequent propagation, possibly through recombination of environmentally driven resistance mutations.

# Triazole resistance in human pathogen *Aspergillus fumigatus* on commercial plant products

Primary Category: Biology and Disease Management

Secondary Category: Mycology

Pathogen Type Keyword: Fungus

Host Type Keyword: Other






Associated Host Type Keyword: Other

Session Type: Research On-Demand

## Talk at APS conference August 2021

- purpose study was to identify if azole-resistant *A. fumigatus* is present on commercial products in the United States
- **10** categories of retail plant products were screened for azole-resistant *A. fumigatus*. Of the approximately **500** isolates that have been collected, **6** from peanut and compost have been identified as pan-azole-resistant through minimum inhibitory concentration (MIC) testing
- mechanism of resistance of azole-resistant isolates will be investigated by *cyp51A* sequencing and population genetic analyses based on STRA<sub>f</sub> genotyping will be conducted to determine the relatedness of strains collected in this study to clinical and environmental strains worldwide

# Identification of Novel Mutations Contributing to Azole Tolerance of *Aspergillus fumigatus* through *In Vitro* Exposure to Tebuconazole

Authors: Takahito Toyotome  , Kenji Onishi, Mio Sato, Yoko Kusuya, Daisuke Hagiwara , Akira Watanabe , and Hiroki Takahashi  : [AUTHORS INFO & AFFILIATIONS](#)

DOI: <https://doi.org/10.1128/AAC.02657-20>  Check for updates

- study from Japan explored genes contributing to azole tolerance in *A. fumigatus* by *in vitro* mutant selection with tebuconazole
- after three rounds of selection, obtained four isolates with low susceptibility to tebuconazole; these isolates also showed low susceptibility to itraconazole and voriconazole.